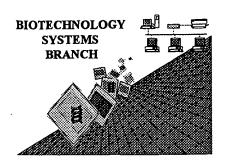# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _08/819,669C_

Art Unit / Team No. : _1644_

Date Processed by STIC: _6/19/99_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

m.Lubet

1644

PAGE:-1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/819,669C*

DATE: 06/19/1999
TIME: 16:48:42

INPUT SET: S32279.raw

> This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5           (i)   APPLICANTS:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
 6                 Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
 7                 Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
 8
 9           (ii) TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
10                 Rejection Antigens and Uses Thereof
11
12           (iii) NUMBER OF SEQUENCES:  26
13
14           (iv) CORRESPONDENCE ADDRESS:
15                 (A) ADDRESSEE: Fulbright & Jaworski LLP
16                 (B) STREET: 666 Fifth Avenue
17                 (C) CITY:  New York City
18                 (D) STATE:  New York
19                 (F) ZIP:  10103
20
21           (v) COMPUTER READABLE FORM:
22                 (A) MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
23                 (B) COMPUTER:  IBM
24                 (C) OPERATING SYSTEM:  PC-DOS
25                 (D) SOFTWARE:  Wordperfect
26
27           (vi) CURRENT APPLICATION DATA:
28                 (A) APPLICATION NUMBER:  08/819,669
29                 (B) FILING DATE: 17-March-1997
30                 (C) CLASSIFICATION:  435
31
32           (vii) PRIOR APPLIATION DATA:
33                 (A) APPLICATION NUMBER: 08/142,368
34                 (B) FILING DATE: 02-MAY-1994
35
36           (vii) PRIOR APPLICATION DATA:
37                 (A) APPLICATION NUMBER:  PCT/US92/04354
38                 (B) FILING DATE:  22-MAY-1992
39
40           (vii) PRIOR APPLICATION DATA:
41                 (A) APPLICATION NUMBER:  07/807,043
42                 (B) FILING DATE:  12-DECEMBER-1991
43
44           (vii) PRIOR APPLICATION DATA:
45                 (A) APPLICATION NUMBER:  07/764,364
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[handwritten annotations:] *→(E) COUNTRY: USA   add the mandatory subheading and response*   *--> ok 30*

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/819,669C*

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46              (B) FILING DATE:   23-SEPTEMBER-1991
47
48        (vii) PRIOR APPLICATION DATA:
49              (A) APPLICATION NUMBER:  07/728,838
50              (b) FILING DATE:   9-JULY-1991
51
52        (vii) PRIOR APPLICATION DATA:
53              (A) APPLICATION NUMBER:  07/705,702
54              (B) FILING DATE:   23-May-1991
55
56        (viii) ATTORNEY/AGENT INFORMATION:
57              (A) NAME:  Hanson, Norman D.
58              (B) REGISTRATION NUMBER:  30,946
59              (C) REFERENCE/DOCKET NUMBER:  LUD 5253.5-US
60
61        (ix) TELECOMMUNICATION INFORMATION:
62              (A) TELEPHONE: (212)318-3168
63              (B) TELEFAX: (212)752-5958
64
65
66
```

ERRORED SEQUENCES FOLLOW:

insert this MANDATORY subheading and its response for all nucleic acid sequences (global error)

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67        (2) INFORMATION FOR SEQ ID NO: 1:
68              (i) SEQUENCE CHARACTERISTICS:
69                  (A) LENGTH:  462 base pairs
70                  (B) TYPE:  nucleic acid      → (C) STRANDEDNESS:
71                  (D) TOPOLOGY:  linear
72              (ii) MOLECULE TYPE:  genomic DNA
-->  73       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 1:
74
75
76
77
78        ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG        60
79        ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT       120
80        CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG       180
81        CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC       240
82        CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT       300
83        AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT       360
84        GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT       420
85        TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                          462
86
87
88
89
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90        (2) INFORMATION FOR SEQ ID NO: 2:
91              (i) SEQUENCE CHARACTERISTICS:
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INPUT SET: S32279.raw

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 92              (A) LENGTH:   675 base pairs
 93              (B) TYPE:  nucleic acid           same gen (STRANDEDNESS:)
 94              (D) TOPOLOGY:  linear
 95         (ii) MOLECULE TYPE:  genomic DNA
 96         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 2:
 97
 98
 99   ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT        48
100   Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
101                       5               10                  15
102   GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA        96
103   Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
104                   20                  25                  30
105   GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA       144
106   Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
107               35                  40                  45
108   AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG       192
109   Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
110           50                  55                  60
111   TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC       240
112   Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
113   65                  70                  75                  80
114   TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC       288
115   Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
116                       85                  90                  95
117   GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       336
118   Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
119                   100                 105                 110
120   GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG       384
121   Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
122               115                 120                 125
123   GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG       432
124   Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
125           130                 135                 140
126   GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG       480
127   Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
128   145                 150                 155                 160
129   AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC       528
130   Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
131                       165                 170                 175
132   CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT       576
133   Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
134                   180                 185                 190
135   GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG       624
136   Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
137               195                 200                 210
138   GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT       672
139   Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
140   220                 225                 230                 235
141
142   TAG                                                                  675
143
144
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/819,669C*

DATE: 06/19/1999
TIME: 16:48:43

INPUT SET: S32279.raw

145

146   (2) INFORMATION FOR SEQ ID NO: 3:
147   (i) SEQUENCE CHARACTERISTICS:
148   (A) LENGTH: 228 base pairs
149   (B) TYPE: nucleic acid
150   (D) TOPOLOGY: linear
151   (ii) MOLECULE TYPE: genomic DNA
--> 152   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
153
154
155
156   GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT   60
157   TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT   120
158   TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC   180
159   ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC   228
160
161

162   (2) INFORMATION FOR SEQ ID NO: 4:
163   (i) SEQUENCE CHARACTERISTICS:
164   (A) LENGTH: 1365 base pairs
165   (B) TYPE: nucleic acid
166   (D) TOPOLOGY: linear
167   (ii) MOLECULE TYPE: genomic DNA
--> 168   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
169
170
171   ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT   50
172   GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT   100
173   CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG   150
174   AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT   200
175   CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA   250
176   CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT   300
177   AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG   350
178   CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG   400
179   CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT   450
180   ACCCTTTGTG CC   462
181   ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA   504
182   GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG   546
183   TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC   588
184   TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC   630
185   ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC   672
186   TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG   714
187   GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC   756
188   GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT   798
189   GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA   840
190   GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA   882
191   GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT   924
192   GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT   966
193   TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG   1008
194   AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT   1050
195   GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG   1092

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196   GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      1134
197   TAG                                                          1137
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199   TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA       1237
200   ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT       1287
201   CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT       1337
202   GTTAAAAATA AAAGTTTGAC TTGCATAC                               1365
203
204
205
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206   (2)  INFORMATION FOR SEQ ID NO: 5:
207          (i)  SEQUENCE CHARACTERISTICS:
208               (A)  LENGTH:   4698  base pairs
209               (B)  TYPE:   nucleic acid
210               (D)  TOPOLOGY:   linear
211          (ii) MOLECULE TYPE:   genomic DNA
212          (xi) SEQUENCE DESCRIPTION:   SEQ ID NO: 5:
213
214   ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT         50
215   GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT        100
216   CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG        150
217   AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT        200
218   CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA        250
219   CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT        300
220   AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG        350
221   CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG        400
222   CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT        450
223   ACCCTTTGTG CC                                                 462
224   ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA       504
225   GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG       546
226   TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC       588
227   TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC       630
228   ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC       672
229   TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG       714
230   GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC       756
231   GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       798
232   GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA       840
233   GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA       882
234   GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                916
235   GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA        966
236   CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC       1016
237   TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC       1066
238   CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC       1116
239   TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC       1166
240   TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC       1216
241   TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC       1266
242   CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT       1316
243   TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT       1366
244   TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT       1416
245   CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG       1466
246   TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT       1516
247   CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT       1566
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/819,669C*

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248	TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCTGGCAC	1616
249	TCACTCTGTA	GACCAGGCTG	GCCTCAAACT	CAGAAATCTG	CCTGCCTCTG	1666
250	CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
251	GCCTTTCTTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
252	AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCCTCC	CCCTCCCTGT	1816
253	TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
254	CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTACCTCTC	CCTGCTTTCT	1916
255	GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966
256	AGCTCACCTT	TTTGTTTGTT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
257	TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCTCCCCC	TCCGGCTTCC	2066
258	CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCCC	TCGCTGGCTC	CCCCTCCCTT	2116
259	TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
260	CTTTTCTAGA	CTCCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
261	CCTGACCCTG	CTCCCCTTCC	CCTCCCAGCT	CCCCCCTCTT	TTCCCACCTC	2266
262	CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316
263	TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
264	GACTTCCTCT	CCAGCCGCCC	AGTTCCCTGC	AGTCCTGGAG	TCTTTCCTGC	2416
265	CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCCT	2466
266	ATGTGTCTCT	CTTCCTATCT	ATCCCTTCCT	TTCTGTCCCC	TCTCCTCTGT	2516
267	CCATCACCTC	TCTCCTCCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566
268	CCTGCTTCTT	TACCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616
269	TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
270	ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
271	TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCCTATG	CCCTCTACTC	2766
272	TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCTTT	CCACCCTGCC	2816
273	CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
274	ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAAA	ATCAGCAGGA	2916
275	AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
276	AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
277	CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
278	CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
279	GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
280	TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
281	TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266
282	GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
283	TTGCTAAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCCAG		3355
284	GT	GTT CCT GGC	CAT CAT TTA	AGG AAG AAT	GAA GTG AAG TGT	3396
285	AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT TTC CTG	GTG TCT	3438
286	ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG TGT AGG	TGT GAA	3480
287	AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG GAA GAA	GAA GAA	3522
288	GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA AAC CCG	GAT GGC	3564
289	TTC TCA CCT	TAG				3576
290	GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA	3626
291	GCTAAGAGCA	TCTTTTTAAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
292	TCTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
293	CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
294	GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
295	GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
296	TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
297	TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTTGTCG	3976
298	TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
299	CTTAAAATTT	CCTTCATCTT	TAATTTTCCT	TAACTTTAGT	TTTTTTCACT	4076
300	TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTTA	GATTTCTTAA	4126

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301  AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA  4176
302  GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA  4226
303  GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC  4276
304  CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC  4326
305  ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT  4376
306  ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA  4426
307  AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC  4476
308  AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT  4526
309  TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA  4576
310  TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT  4626
311  GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA  4676
312  AATAAAAGTT TGACTTGCAT AC                                4698
313
314
315
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330  (2) INFORMATION FOR SEQ ID NO: 7:   2419 shown (next page)
331       (i) SEQUENCE CHARACTERISTICS:
332           (A) LENGTH: 2418 base pairs              same
333           (B) TYPE:   nucleic acid              STRANDEDNESS
334           (D) TOPOLOGY: linear                   err, too
335       (ii) MOLECULE TYPE: genomic DNA
336       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
337
338
339  GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG    50
340  GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC   100
341  TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG   150
342  GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT   200
343  TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT   250
344  GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA   300
345  CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT   350
346  CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC   400
347  TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC   450
348  CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG   500
349  TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT   550
350  CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT   600
351  GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC   650
352  ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG   700
353  GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC   750
354  CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC   800
355  AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA   850
356  CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG   900
357  TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT   950
358  TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG  1000
359  GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA  1050
360  GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG  1100
361  TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA  1150
362  GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC  1200
363  AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG  1250
364  CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT  1300
365  GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA  1350
366  TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC  1400
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INPUT SET: S32279.raw

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    367   CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT    1450
    368   ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTTCGCTTT    1500
    369   TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT    1550
    370   CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC    1600
    371   ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG    1650
    372   CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCTCAGT AGTAGGTTTC    1700
    373   TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT    1750
    374   TCAAATGTTT TTTTTTAAGG GATGGTTGAA TGAACTTCAG CATCCAAGTT    1800
    375   TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA    1850
    376   GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG    1900
    377   ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA    1950
    378   AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC    2000
    379   CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG    2050
    380   GATTTCCTTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG    2100
    381   AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC    2150
    382   TTTTTGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT    2200
    383   CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG    2250
    384   AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA    2300
    385   GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG    2350
    386   GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT    2400
--> 387   AATGATCTTG GGTGGATCC                                       2418  2419
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    389
    390
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    391   (2) INFORMATION FOR SEQ ID NO: 8:
    392         (i) SEQUENCE CHARACTERISTICS:
--> 393             (A) LENGTH:  5724 base pairs        5674 shown (next page)
    394             (B) TYPE:   nucleic acid            same "STRANDEDNESS" error
    395             (D) TOPOLOGY:  linear
    396        (ii) MOLECULE TYPE:  genomic DNA
    397        (ix) FEATURE:
    398             (A) NAME/KEY:  MAGE-1 gene
--> 399        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 8:
    400
    401
    402   CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT          50
    403   TACGCCACCC ATCCAAACAT CTTCACGCTC ACCCCCAGCC CAAGCCAGGC         100
    404   AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG         150
    405   ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT         200
    406   CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG         250
    407   TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC         300
    408   AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT         350
    409   GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA         400
    410   CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG         450
    411   AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG         500
    412   AGGGCTGAGG GTCCCTAAGA CCCCACTCCC GTGACCCAAC CCCCACTCCA         550
    413   ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA         600
    414   CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC         650
    415   ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC         700
    416   CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC         750
    417   GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG         800
    418   AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG         850
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INPUT SET: S32279.raw

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419   AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA    900
420   GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCCACC    950
421   CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG   1000
422   CCTTGAGAGA CACCAGGTTC TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC   1050
423   TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA   1100
424   GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC   1150
425   ACTCCAATCC CCACTCCCAC CCCATTCGCA TTCCCATTCC CCACCCAACC   1200
426   CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA   1250
427   CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACCC TTCTGCCACC   1300
428   TCACCCTCAC TGCCCCCAAC CCCACCCTCA TCTCTCTCAT GTGCCCCACT   1350
429   CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTTTGCCCC TGCTCTCAAC   1400
430   CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC   1450
431   AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG   1500
432   ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG   1550
433   CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCAAAATG   1600
434   ATCCAGTACC ACCCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT   1650
435   GTCTCAGCTG GACCACCCCC CGTCCCGTCC CACTGCCACT TAACCCACAG   1700
436   GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTCAGGAGA   1750
437   GGCAGGGCCC AGGCATCAAG GTCCAGCATC CGCCCGGCAT TAGGGTCAGG   1800
438   ACCCTGGGAG GGAACTGAGG GTTCCCCACC CACACCTGTC TCCTCATCTC   1850
439   CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCCAACCTCA   1900
440   TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC   1950
441   CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG   2000
442   GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA   2050
443   GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG   2100
444   ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA   2150
445   TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA   2200
446   GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT   2250
447   GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT CCTGCATCTT   2300
448   TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC   2350
449   AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG   2400
450   AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG   2450
451   CTGTCCCCTT TTAGTAGCTC TAGGGGACC AGATCAGGGA TGGCGGTATG   2500
452   TTCCATTCTC ACTTGTACCA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG   2550
453   ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGAATTGGG   2600
454   GGTTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT GAGACAGACA   2650
455   AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTCAGC CCTGGACACC   2700
456   TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTTCCAGA TCTGGGGCAG   2750
457   GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA GGGACCCCCA   2800
458   TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG TTCGGGTGAG   2850
459   GAACATGAGG GAGGACTGAG GGTACCCCAG GACCAGAACA CTGAGGGAGA   2900
460   CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCCAGAG AGCATGGGCT   2950
461   GGGCCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT GATGTCAGGG   3000
462   ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG TAGAGGGAGC   3050
463   GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG GCACCTCACC   3150
464   CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT GCCCTTCCCC   3200
465   AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCCTCCT GTCCTTCCAT   3250
466   TCCTTATCAT GGATGTGAAC TCTTGATTTG GATTTCTCAG ACCAGCAAAA   3300
467   GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGCGTGAGAA   3350
468   CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GAGTCCAGCC   3400
469   CACCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GGTCTGCACC   3450
470   CTGAGGGCCC GTGGATTCCT CTTCCTGGAG CTCCAGGAAC CAGGCAGTGA   3500
471   GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG   3550
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(handwritten annotations: 3100, 3150 number, arrow marks near lines 463–464)

INPUT SET: S32279.raw

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472   GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC      3600
473   TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG      3650
474   TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCCT      3700
475   CTCACTTCCT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG      3750
476   ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT GTAAGTAGGC      3800
477   CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC      3850
478   TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT CCTGCCCACA      3900
479   CTCCTGCCTG CTGCCCTGAC GAGAGTCATC                           3930
480   ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA     3972
481   GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG     4014
482   CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC     4056
483   CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG     4098
484   AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC     4140
485   ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA     4182
486   GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC     4224
487   CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT     4266
488   CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA     4308
489   GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT     4350
490   CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC     4392
491   TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC     4434
492   TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG     4476
493   CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA     4518
494   ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT     4560
495   GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT     4602
496   GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG     4644
497   CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC     4686
498   AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG     4728
499   GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA                 4761
500   AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC               4800
501   GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG      4850
502   GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC      4900
503   AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC TCGTGTGACA      4950
504   TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG      5000
505   GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA      5050
506   ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC      5100
507   AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG      5150
508   TAAGAGTCTT GTGTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA      5200
509   TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG      5250
510   CAGTAAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT      5300
511   CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTTAAAG ATATATGCAT      5350
512   ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA      5400
513   TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA      5450
514   TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC      5500
515   AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTCACGT      5550
516   AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG      5600
517   GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA      5650
518   GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT GGGGGAGCTG      5700
519   ATTGTAATGA TCTTGGGTGG ATCC                                  5724
520
521
522
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523   (2) INFORMATION FOR SEQ ID NO: 9:

INPUT SET: S32279.raw

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524       (i) SEQUENCE CHARACTERISTICS:
525            (A) LENGTH:  4157 base pairs
526            (B) TYPE:    nucleic acid
527            (D) TOPOLOGY:  linear
528      (ii) MOLECULE TYPE:  genomic DNA
529      (ix) FEATURE:
530            (A) NAME/KEY:  MAGE-2 gene
-->  531  (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 9:
532
533
534

535   CCCATCCAGA TCCCCATCCG GGCAGAATCC GGTTCCACCC TTGCCGTGAA        50
536   CCCAGGGAAG TCACGGGCCC GGATGTGACG CCACTGACTT GCACATTGGA       100
537   GGTCAGAGGA CAGCGAGATT CTCGCCCTGA GCAACGGCCT GACGTCGGCG       150
538   GAGGGAAGCA GGCGCAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG       200
539   AGGACTGAGG CGGGCCTCAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC       250
540   GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAGGGGAA GACTTCTCAG       300
541   GCTCAGTCGC CACCACCTCA CCCCGCCACC CCCCGCCGCT TTAACCGCAG       350
542   GGAACTCTGG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAAG       400
543   TGCTCAGGGC CCAGACTCAG CCAGGAATCA AGGTCAGGAC CCCAAGAGGG       450
544   GACTGAGGGC AACCCACCCC CTACCCTCAC TACCAATCCC ATCCCCCAAC       500
545   ACCAACCCCA CCCCCATCCC TCAAACACCA ACCCCACCCC CAAACCCCAT       550
546   TCCCATCTCC TCCCCCACCA CCATCCTGGC AGAATCCGGC TTTGCCCCTG       600
547   CAATCAACCC ACGGAAGCTC CGGGAATGGC GGCCAAGCAC GCGGATCCTG       650
548   ACGTTCACAT GTACGGCTAA GGGAGGGAAG GGGTTGGGTC TCGTGAGTAT       700
549   GGCCTTTGGG ATGCAGAGGA AGGGCCCAGG CCTCCTGGAA GACAGTGGAG       750
550   TCCTTAGGGG ACCCAGCATG CCAGGACAGG GGGCCCACTG TACCCCTGTC       800
551   TCAAACTGAG CCACCTTTTC ATTCAGCCGA GGGAATCCTA GGGATGCAGA       850
552   CCCACTTCAG GGGGTTGGGG CCCAGCCTGC GAGGAGTCAA GGGGAGGAAG       900
553   AAGAGGGAGG ACTGAGGGGA CCTTGGAGTC CAGATCAGTG GCAACCTTGG       950
554   GCTGGGGGAT CCTGGGCACA GTGGCCGAAT GTGCCCCGTG CTCATTGCAC      1000
555   CTTCAGGGTG ACAGAGAGTT GAGGGCTGTG GTCTGAGGGC TGGGACTTCA      1050
556   GGTCAGCAGA GGGAGGAATC CCAGGATCTG CCGGACCCAA GGTGTGCCCC      1100
557   CTTCATGAGG ACTCCCCATA CCCCCGGCCC AGAAAGAAGG GATGCCACAG      1150
558   AGTCTGGAAG TAAATTGTTC TTAGCTCTGG GGGAACCTGA TCAGGGATGG      1200
559   CCCTAAGTGA CAATCTCATT TGTACCACAG GCAGGAGGTT GGGGAACCCT      1250
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561   GGTTCCCCCT TGAGAAAGGG CAGTCCCTGG CAGGAGTAAA GATGAGTAAC      1350
562   CCACAGGAGG CCATCATAAC GTTCACCCTA GAACCAAAGG GGTCAGCCCT      1400
563   GGACAACGCA CGTGGGGTAA CAGGATGTGG CCCCTCCTCA CTTGTCTTTC      1450
564   CAGATCTCAG GGAGTTGATG ACCTTGTTTT CAGAAGGTGA CTCAGTCAAC      1500
565   ACAGGGGCCC CTCTGGTCGA CAGATGCAGT GGTTCTAGGA TCTGCCAAGC      1550
566   ATCCAGGTGG AGAGCCTGAG GTAGGATTGA GGGTACCCCT GGGCCAGAAT      1600
567   GCAGCAAGGG GGCCCCATAG AAATCTGCCC TGCCCCTGCG GTTACTTCAG      1650
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571   GACTCGTCAC CCAGGACACC TGGACTCCAA TGAATTTGAC ATCTCTCGTT      1850
572   GTCCTTCGCG GAGGACCTGG TCACGTATGG CCAGATGTGG GTCCCCTCTA      1900
573   TCTCCTTCTG TACCATATCA GGGATGTGAG TTCTTGACAT GAGAGATTCT      1950
574   CAAGCCAGCA AAAGGGTGGG ATTAGGCCCT ACAAGGAGAA AGGTGAGGGC      2000
575   CCTGAGTGAG CACAGAGGGG ACCCTCCACC CAAGTAGAGT GGGGACCTCA      2050
576   CGGAGTCTGG CCAACCCTGC TGAGACTTCT GGGAATCCGT GGCTGTGCTT      2100
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577   GCAGTCTGCA CACTGAAGGC CCGTGCATTC CTCTCCCAGG AATCAGGAGC        2150
578   TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC CTCAGGTCAC        2200
579   AGAGCAGAGG GGACGCAGAC AGTGCCAACA CTGAAGGTTT GCCTGGAATG        2250
580   CACACCAAGG GCCCCACCCG CCCAGAACAA ATGGGACTCC AGAGGGCCTG        2300
581   GCCTCACCCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCCGG        2350
582   CTGTACCCTG AGGTGCCCTC CCACTTCCTC CTTCAGGTTC TGAGGGGGAC        2400
583   AGGCTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA AGGAGAAGAT        2450
584   CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTTCAGTTC AGTTCTCACC        2500
585   TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG        2550
586   CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATC         2597
587   ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA        2639
588   GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG        2681
589   CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT        2723
590   TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC        2765
591   GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC        2807
592   TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT        2849
593   GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT        2891
594   CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG        2933
595   ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC        2975
596   AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC        3017
597   AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC        3059
598   TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA        3101
599   GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG        3143
600   GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG        3185
601   CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA        3227
602   ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG AGG AGG        3269
603   CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC        3311
604   TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG        3353
605   GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT        3395
606   GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA        3437
607   ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT        3479
608   GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT        3521
609   TTG AGA GAG GGA GAA GAG TGA                                    3542
610   GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT        3592
611   GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA        3642
612   GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG        3692
613   TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA        3742
614   TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA        3792
615   GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG        3842
616   TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG        3892
617   TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG        3942
618   AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAGAT AGTTAATTCT         3992
619   TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT        4042
620   TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT        4092
621   TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC        4142
622   CCTGGTAGTA GTGGG                                               4157
623
624
625
626
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627   (2) INFORMATION FOR SEQ ID NO: 10:
628       (i) SEQUENCE CHARACTERISTICS:
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INPUT SET: S32279.raw

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629            (A) LENGTH:   662 base pairs
630            (B) TYPE:    nucleic acid
631            (D) TOPOLOGY:  linear
632       (ii) MOLECULE TYPE:  genomic DNA
633       (ix) FEATURE:
634            (A) NAME/KEY:  MAGE-21 gene
635       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 10:
636
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639   GGATCCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC        50
640   AGGGAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT       100
641   CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG       150
642   GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG       200
643   ACTGAGGCGG GCCTCACCCC AGACAGAGGG CCCCCAATAA TCCAGCGCTG       250
644   CCTCTGCTGC CAGGCCTGGA CCACCCTGCA GGGGAAGACT TCTCAGGCTC       300
645   AGTCGCCACC ACCTCACCCC GCCACCCCCC GCCGCTTTAA CCGCAGGGAA       350
646   CTCTGGTGTA AGAGCTTTGT GTGACCAGGG CAGGGCTGGT TAGAAGTGCT       400
647   CAGGGCCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCA AGAGGGGACT       450
648   GAGGGTAACC CCCCCGCACC CCCACCACCA TTCCCATCCC CCAACACCAA       500
649   CCCCACCCCC ATCCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA       550
650   ACGGCACCCC CAAACCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG       600
651   GAGCTTTGCC CCTGCAATCA ACCCACGGAA GCTCCGGGAA TGGCGGCCAA       650
652   GCACGCGGAT CC                                               662
653
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655
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656   (2) INFORMATION FOR SEQ ID NO: 11:
657       (i) SEQUENCE CHARACTERISTICS:
658            (A) LENGTH:   1640 base pairs
659            (B) TYPE:    nucleic acid
660            (D) TOPOLOGY:  linear
661       (ii) MOLECULE TYPE:  cDNA to mRNA
662       (ix) FEATURE:
663            (A) NAME/KEY:  cDNA MAGE-3
664       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 11:
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667   GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG        50
668   GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA       100
669   AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCCAC ACTCCCGCCT       150
670   GTTGCCCTGA CCAGAGTCAT C                                     171
671   ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA     213
672   GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG     255
673   CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT     297
674   TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC     339
675   GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC     381
676   CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT     423
677   GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC     465
678   CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG     507
679   GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC     549
680   AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC     591
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INPUT SET: S32279.raw

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682    TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA        675
683    GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG        717
684    GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG        759
685    CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA        801
686    AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG        843
687    CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG        885
688    TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG        927
689    GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT        969
690    GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA       1011
691    ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT       1053
692    GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT       1095
693    TTG AGA GAG GGG GAA GAG TGA                                   1116
694    GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT       1166
695    GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA       1216
696    GGCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG       1266
697    TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG       1316
698    TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG       1366
699    GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG       1416
700    TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA       1466
701    TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC       1516
702    GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG       1566
703    ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA       1616
704    ACCAGGATTT CCTTGACTTC TTTG                                   1640
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709    (2) INFORMATION FOR SEQ ID NO: 12:
710         (i) SEQUENCE CHARACTERISTICS:
711              (A) LENGTH:  943 base pairs
712              (B) TYPE:    nucleic acid
713              (D) TOPOLOGY:  linear
714         (ii) MOLECULE TYPE:  genomic DNA
715         (ix) FEATURE:
716              (A) NAME/KEY:  MAGE-31 gene
717         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 12:
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720    GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT         50
721    CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG        100
722    GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG        150
723    AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA        200
724    GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC        250
725    CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT        300
726    TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC        350
727    CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC        400
728    AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG        450
729    TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC        500
730    TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCACA        550
731    CTCCCGCCTG TTGCCCTGAC CAGAGTCATC                             580
732    ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA        622
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733  GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG          664
734  CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT          706
735  TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC          748
736  GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC          790
737  CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT          832
738  GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC          874
739  CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG          916
740  GTG GCC AAG TTG GTT CAT TTT CTG CTC                              943
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744
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745  (2) INFORMATION FOR SEQ ID NO: 13:
746       (i) SEQUENCE CHARACTERISTICS:
747            (A) LENGTH:  2531 base pairs
748            (B) TYPE:    nucleic acid
749            (D) TOPOLOGY:  linear
750       (ii) MOLECULE TYPE:  genomic DNA
751       (ix) FEATURE:
752            (A) NAME/KEY:  MAGE-4 gene
753       (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 13:
754
755
756  GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG         50
757  GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC        100
758  TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG        150
759  GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT        200
760  TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT        250
761  GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA        300
762  CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT        350
763  CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA        400
764  CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC        450
765  TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT        500
766  TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC        550
767  TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG        600
768  CCTGCTGCCC TGACCAGAGT CATC                                     624
769  ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA        666
770  GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA        708
771  CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC        750
772  TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT        792
773  GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT        834
774  GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC        876
775  AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC        918
776  TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC        960
777  AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA       1002
778  GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC       1044
779  ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA       1086
780  GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG       1128
781  GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC       1170
782  CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC       1212
783  TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT       1254
784  GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG       1296
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785   GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT         1338
786   GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG         1380
787   CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT         1422
788   CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT         1464
789   GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC         1506
790   AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA         1548
791   GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                         1578
792   GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC          1628
793   ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC          1678
794   CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT          1728
795   TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT          1778
796   GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT          1828
797   TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG          1878
798   AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG          1928
799   GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT          1978
800   GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA          2028
801   GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG          2078
802   CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA          2128
803   ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC          2178
804   AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA          2228
805   GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT          2278
806   CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT          2328
807   GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA          2378
808   AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC          2428
809   AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC          2478
810   TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT          2528
811   GGG                                                             2531
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816   (2) INFORMATION FOR SEQ ID NO: 14:
817        (i) SEQUENCE CHARACTERISTICS:
818             (A) LENGTH:  2531 base pairs
819             (B) TYPE:   nucleic acid
820             (D) TOPOLOGY:  linear
821        (ii) MOLECULE TYPE:  genomic DNA
822        (ix) FEATURE:
823             (A) NAME/KEY:  MAGE-41 gene
824        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 14:
825
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827   GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG           50
828   GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC          100
829   TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG          150
830   GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT          200
831   TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT          250
832   GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA          300
833   CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT          350
834   CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA          400
835   CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC          450
836   TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT          500
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INPUT SET: S32279.raw

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837  TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC          550
838  TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG          600
839  CCTGCTGCCC TGAGCAGAGT CATC                                      624
840  ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA         666
841  GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG         708
842  CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC         750
843  TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT         792
844  GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT         834
845  GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC         876
846  AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC         918
847  TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC         960
848  AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA         1002
849  GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC         1044
850  ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA         1086
851  GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG         1128
852  GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC         1170
853  CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC         1212
854  TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT         1254
855  GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG         1296
856  GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT         1338
857  GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG         1380
858  CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT         1422
859  CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT         1464
860  GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC         1506
861  AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA         1548
862  GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                         1578
863  GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC          1628
864  ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC          1678
865  CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT          1728
866  TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT          1778
867  GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT          1828
868  TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG          1878
869  AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG          1928
870  GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT          1978
871  GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA          2028
872  GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG          2078
873  CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA          2128
874  ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC          2178
875  AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA          2228
876  GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT          2278
877  CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT          2328
878  GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA          2378
879  AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC          2428
880  AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC          2478
881  TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT          2528
882  GGG                                                             2531
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886  (2) INFORMATION FOR SEQ ID NO: 15:
887      (i) SEQUENCE CHARACTERISTICS:
888          (A) LENGTH:  1068 base pairs
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PAGE: 18

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999
TIME: 16:48:48

INPUT SET: S32279.raw

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889        (B) TYPE:   nucleic acid
890        (D) TOPOLOGY:  linear
891    (ii) MOLECULE TYPE:  cDNA to mRNA
892    (ix) FEATURE:
893        (A) NAME/KEY:  cDNA MAGE-4
894    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 15:
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896
897
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898     G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA                82
899    GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG              124
900    CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA              166
901    ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT              208
902    GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT              250
903    GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC              292
904    ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG              334
905    GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC              376
906    GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG              418
907    GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT              460
908    GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC              502
909    ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG .            544
910    GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT              586
911    CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG              628
912    CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA              670
913    TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC              720
914    TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG             770
915    TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTGTT GTAACATGAG             820
916    GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG             870
917    GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA             920
918    ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA             970
919    AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT            1020
920    AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT            1068
921    TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC
922
923
924
925
926    (2) INFORMATION FOR SEQ ID NO: 16:
927        (i) SEQUENCE CHARACTERISTICS:
928            (A) LENGTH:  2226 base pairs
929            (B) TYPE:   nucleic acid
930            (D) TOPOLOGY:  linear
931        (ii) MOLECULE TYPE:  genomic DNA
932        (ix) FEATURE:
933            (A) NAME/KEY:  MAGE-5 gene
934        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 16:
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937    GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG             100
938    GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC             150
939    TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG             200
940    GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT
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      942   TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC       300
      943   GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG       350
      944   TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT       400
      945   CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG       450
      946   GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG       500
      947   ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA       550
      948   GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC       600
      949   AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC           644
-->   950   ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA/      684 686
-->   951   CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG'      728 OK
      952   GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA       770
      953   TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA       812
      954   AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC       854
      955   CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG       896
      956   TGG CTG ACT TGA                                             908
      957   TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA       958
      958   GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT      1008
      959   CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA      1058
      960   AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA      1108
      961   CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG      1158
      962   GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG CAAATGCGTC      1208
      963   CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG      1258
      964   GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT      1308
      965   TGGTGCAGGA AAACTACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC      1358
      966   ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA      1408
      967   CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC      1458
      968   CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG      1508
      969   CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG      1558
      970   CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC      1608
      971   TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT TCTGTTCTAT      1658
      972   TGGATGACTT TGAGATTTGT CTTTGTTTCC TTTTGGAATT GTTCAAATGT      1708
      973   TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA      1758
      974   CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT      1808
      975   TTTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT      1858
      976   TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAAC      1908
      977   TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC      1958
      978   TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCTTGGC      2008
      979   TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT      2058
      980   TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTGCTC  TGTGGAAGGC      2108
      981   CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA      2158
      982   CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT      2208
      983   GCCCTCTAAG ATGTAGAG                                        2226
      984
      985
      986
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      987   (2) INFORMATION FOR SEQ ID NO: 17:
      988        (i) SEQUENCE CHARACTERISTICS:
      989            (A) LENGTH:  2305 base pairs
      990            (B) TYPE:   nucleic acid
      991            (D) TOPOLOGY: linear
      992        (ii) MOLECULE TYPE: genomic DNA
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PAGE: 20

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/819,669C

DATE: 06/19/1999
TIME: 16:48:48

INPUT SET: S32279.raw

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993         (ix) FEATURE:
994              (A) NAME/KEY:  MAGE-51 gene
-->  995         (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 17:
996
997
998                                                                          50
999     GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG              100
1000    GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC              150
1001    TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG              200
1002    GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT              250
1003    TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC              300
1004    TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC              350
1005    GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG              400
1006    TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT              450
1007    CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG              500
1008    GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG              550
1009    ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTGGGTC TTTTAGCTGA              600
1010    GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC              644
1011    AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC                    686
1012    ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA            728
1013    GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC            770
1014    AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT            812
1015    CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG            854
1016    GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA            896
1017    TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA            938
1018    AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC            980
1019    CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG            992
1020    TGG CTG ACT TGA                                                   1042
1021    TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA             1092
1022    GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TTCCTGAGAT             1142
1023    CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA             1192
1024    AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGCCCAA GACGGGCCTC             1242
1025    CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC             1292
1026    CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA             1342
1027    GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG             1392
1028    AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG             1442
1029    CAGGAAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC             1492
1030    TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG             1542
1031    CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCTACC CATCCCTGCA             1592
1032    TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCACCTTCC AGGGCTCCGT             1642
1033    CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT             1692
1034    CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCATT CTTCTCTCTT             1742
1035    TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG             1792
1036    ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCCTTT             1842
1037    TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG             1892
1038    TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA             1942
1039    TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC             1992
1040    AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAACTGATGA             2042
1041    GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC             2092
1042    GGTAAAATTT TTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT              2142
1043    TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT             2192
1044    GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG             2242
1045    GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG
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INPUT SET: S32279.raw

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1046    TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT         2292
1047    CTAAGATGTA GAG                                                2305
1048
1049
1050
1051
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1052    (2) INFORMATION FOR SEQ ID NO: 18:
1053          (i) SEQUENCE CHARACTERISTICS:
1054                (A) LENGTH:   225 base pairs
1055                (B) TYPE:    nucleic acid
1056                (D) TOPOLOGY:  linear
1057          (ii) MOLECULE TYPE:  cDNA
1058          (ix) FEATURE:
1059                (A) NAME/KEY:  MAGE-6 gene
-->  1060    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 18:
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1062
1063    TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG            42
1064    CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC            84
1065    GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC           126
1066    GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC           168
1067    TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC           210
1068    TGT GCC CCT GAG GAG                                               225
1069
1070
1071
1072
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1073    (2) INFORMATION FOR SEQ ID NO: 19:
1074          (i) SEQUENCE CHARACTERISTICS:
1075                (A) LENGTH:   1947 base pairs
1076                (B) TYPE:    nucleic acid
1077                (D) TOPOLOGY:  linear
1078          (ii) MOLECULE TYPE:  genomic DNA
1079          (ix) FEATURE:
1080                (A) NAME/KEY:  MAGE-7 gene
-->  1081    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 19:
1082
1083
1084    TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA           50
1085    GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC          100
1086    TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA          150
1087    GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC          200
1088    ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT          250
1089    GGTTCACAAA TGAGGCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG          300
1090    GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA          350
1091    CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG          400
1092    GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG          450
1093    GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA          500
1094    AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA          550
1095    GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA          600
1096    GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC          650
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INPUT SET: S32279.raw

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1097  TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA                     685
1098  ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT   727
1099  ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA   769
1100  GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT   811
1101  GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC   853
1102  ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA   895
1103  CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC   937
1104  AGA GCA TGC CCG AGA CCG GCC TTC TGA                       964
1105  TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG    1014
1106  GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT    1064
1107  TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC    1114
1108  TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT    1164
1109  CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG    1214
1110  AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG    1264
1111  CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC    1314
1112  AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC    1364
1113  CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT    1414
1114  CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG    1464
1115  GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC    1514
1116  GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA AATGTTCCTT    1564
1117  TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG    1614
1118  GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT    1664
1119  TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG    1714
1120  CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG    1764
1121  GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG    1814
1122  CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA    1864
1123  GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA    1914
1124  AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG                      1947
1125
1126
1127
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1128 (2) INFORMATION FOR SEQ ID NO: 20:
1129   (i) SEQUENCE CHARACTERISTICS:
1130   (A) LENGTH: 1810 base pairs
1131   (B) TYPE: nucleic acid
1132   (D) TOPOLOGY: linear
1133   (ii) MOLECULE TYPE: genomic DNA
1134   (ix) FEATURE:
1135   (A) NAME/KEY: MAGE-8 gene
--> 1136   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
1137
1138
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1139  GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA    50
1140  TCACAGAGCA TAAGAGGCCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT    100
1141  GTTTCCCCTG TATGTATACC AGAGGCCCCT CTGGCATCAG AACAGCAGGA    150
1142  ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG    200
1143  GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA    250
1144  GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGGAAGCA     300
1145  CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA    350
1146  CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT    400
1147  CAATTGCCCA GCTCCGGCCC ACACTCTCCT GCTGCCCTGA CCTGAGTCAT    450
1148  C                                                         451
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INPUT SET: S32279.raw

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1149  ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA      493
1150  GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG      535
1151  CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC      577
1152  TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT      619
1153  GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT      661
1154  TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT      703
1155  GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC      745
1156  CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT      787
1157  GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA      829
1158  TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG      871
1159  AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC      913
1160  AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT      955
1161  GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC      997
1162  ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT     1039
1163  CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC     1081
1164  ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC     1123
1165  TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA                 1156
1166  TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG     1206
1167  AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT     1256
1168  CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG     1306
1169  CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA     1356
1170  TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT     1406
1171  TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG     1456
1172  GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCCT GCTCTGTTAC     1506
1173  ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA     1556
1174  GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC     1606
1175  AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG     1656
1176  AATTGTTCCA ATGTTCCTTC TAATGGATGG TGTAATGAAC TTCAACATTC     1706
1177  ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTTATA TAGTTTAGGA     1756
1178  GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA     1806
1179  ATTC                                                       1810
1180
1181
1182
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1183  (2) INFORMATION FOR SEQ ID NO: 21:
1184        (i) SEQUENCE CHARACTERISTICS:
1185              (A) LENGTH:  1412 base pairs
1186              (B) TYPE:    nucleic acid
1187              (D) TOPOLOGY:  linear
1188        (ii) MOLECULE TYPE:  genomic DNA
1189        (ix) FEATURE:
1190              (A) NAME/KEY:  MAGE-9 gene
1191        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 21:
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1193
1194  TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC       50
1195  AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT      100
1196  GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG      150
1197  TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC      200
1198  TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA      250
1199  GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT      300
1200  TGTTAGAACC TCCAAGGTTC GGTTCTCAGC TGAAGTCTCT CACACACTCC      350
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INPUT SET: S32279.raw

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1201   CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC        400
1202   CTGACTGCTG CCCTGACCAG AGTCATC                                  427
1203   ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA        469
1204   GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA        511
1205   CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT        553
1206   GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT        595
1207   CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC        637
1208   GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC        679
1209   AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT        721
1210   CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG        763
1211   GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG        805
1212   GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA        847
1213   AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC        889
1214   GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG        931
1215   GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC        973
1216   CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC       1015
1217   AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC       1057
1218   AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG       1099
1219   AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC       1141
1220   GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA       1183
1221   AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG       1225
1222   CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC       1267
1223   AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA       1309
1224   AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG       1351
1225   GGA GAG GAG CAA GAG GGA GTC TGA                               1375
1226   GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA                      1412
1227
1228
1229
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1230   (2) INFORMATION FOR SEQ ID NO: 22:
1231        (i) SEQUENCE CHARACTERISTICS:
1232            (A) LENGTH:   920 base pairs
1233            (B) TYPE:    nucleic acid
1234            (D) TOPOLOGY:  linear
1235        (ii) MOLECULE TYPE:  genomic DNA
1236        (ix) FEATURE:
1237            (A) NAME/KEY:  MAGE-10 gene
1238        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 22:
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1240
1241   ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC ACCTACCCTA         50
1242   CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT        100
1243   CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA        150
1244   AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT        200
1245   GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA        250
1246   CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC        300
1247   ACACTCCCAC CTGCTACCCT GATCAGAGTC ATC                          333
1248   ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA       375
1249   GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA       417
1250   CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT       459
1251   TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC       501
1252   TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC       543
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INPUT SET: S32279.raw

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1253   CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC        585
1254   CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT        627
1255   TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA        669
1256   AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT        711
1257   GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT        753
1258   TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG        795
1259   ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT        837
1260   GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC        879
1261   ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC        920
1262
1263
1264
1265
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1266   (2) INFORMATION FOR SEQ ID NO: 23:
1267          (i) SEQUENCE CHARACTERISTICS:
1268               (A) LENGTH:   1107 base pairs
1269               (B) TYPE:   nucleic acid
1270               (D) TOPOLOGY:   linear
1271          (ii) MOLECULE TYPE:  genomic DNA
1272          (ix) FEATURE:
1273               (A) NAME/KEY:  MAGE-11 gene
1274          (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 23:
1275
1276
1277   AGAGAACAGG  CCAACCTGGA  GGACAGGAGT  CCCAGGAGAA  CCCAGAGGAT        50
1278   CACTGGAGGA  GAACAAGTGT  AAGTAGGCCT  TTGTTAGATT  CTCCATGGTT       100
1279   CATATCTCAT  CTGAGTCTGT  TCTCACGCTC  CCTCTCTCCC  CAGGCTGTGG       150
1280   GGCCCCATCA  CCCAGATATT  TCCCACAGTT  CGGCCTGCTG  ACCTAACCAG       200
1281   AGTCATCATG  CCTCTTGAGC  AAAGAAGTCA  GCACTGCAAG  CCTGAGGAAG       250
1282   CCTTCAGGCC  CAAGAAGAAG  ACCTGGGCCT  GGTGGGTGCA  CAGGCTCTCC       300
1283   AAGCTGAGGA  GCAGGAGGCT  GCCTTCTTCT  CCTCTACTCT  GAATGTGGGC       350
1284   ACTCTAGAGG  AGTTGCCTGC  TGCTGAGTCA  CCAAGTCCTC  CCCAGAGTCC       400
1285   TCAGGAAGAG  TCCTTCTCTC  CCACTGCCAT  GGATGCCATC  TTTGGGAGCC       450
1286   TATCTGATGA  GGGCTCTGGC  AGCCAAGAAA  AGGAGGGGCC  AAGTACCTCG       500
1287   CCTGACCTGA  TAGACCCTGA  GTCCTTTTCC  CAAGATATAC  TACATGACAA       550
1288   GATAATTGAT  TTGGTTCATT  TATTCTCCGC  AAGTATCGAG  TCAAGGGGCT       600
1289   GATCACAAAG  GCAGAA                                              616
1290   ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT        658
1291   GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT        700
1292   GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT        742
1293   GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG        784
1294   TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA        826
1295   GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA        868
1296   GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT        910
1297   GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT        952
1298   ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG        994
1299   GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT       1036
1300   CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG       1078
1301   TAC ATA GCC AAT GCC AAT GGG AGG GAT CC                        1107
1302
1303
1304
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       1305    (2) INFORMATION FOR SEQ ID NO: 24:
       1306          (i) SEQUENCE CHARACTERISTICS:
       1307                (A) LENGTH:   2150 base pairs
       1308                (B) TYPE:    nucleic acid
       1309                (D) TOPOLOGY:   linear
       1310          (ii) MOLECULE TYPE:  genomic DNA
       1311          (ix) FEATURE:
       1312                (A) NAME/KEY:  smage-I
  -->  1313          (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 24:
       1314
       1315
       1316
       1317    TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT        50
       1318    CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC       100
       1319    ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC       150
       1320    TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT       200
       1321    GCCCTTGTAT GCAGGCCTAA GTTTTTCTGT CTGCTTAACC CCTCCAAGTG       250
       1322    AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT       300
       1323    ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG       350
       1324    AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCCTAG AAAG           394
       1325    ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT       436
       1326    CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT       478
       1327    TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT       520
  -->  1328    AGT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG       565
  -->  1329    AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG       6040
       1330    GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT       646
       1331    TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT       688
       1332    TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA       730
       1333    GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT       772
       1334    GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA       814
       1335    GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG       856
       1336    AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG       898
       1337    ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT       940
       1338    AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA       982
       1339    ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG      1024
       1340    GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA      1066
       1341    CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG      1108
       1342    TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC      1150
       1343    TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA      1192
       1344    TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG      1234
       1345    ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG      1276
  -->  1346    GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC      1314
  -->  1347    CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA      1360
       1348    ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT      1402
       1349    GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT      1444
       1350    CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA      1486
       1351    GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT      1528
       1352    AAC ATG TAG                                                 1537
       1353    TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG      1587
       1354    AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCTGTTAT      1637
       1355    ACATTAGTAG AATGGAGGCT ATTTTTGTTA CTTTTCAAAT GTTTGTTTAA      1687
       1356    CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC      1737
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INPUT SET: S32279.raw

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1357   TGTCACTTGT CAGATTAGGA CTTGTTTTGT TATTTGCAAC AAACTGGAAA          1787
1358   ACATTATTTT GTTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG          1837
1359   GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG          1887
1360   GGAAAGTTTA TATTGTTAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA          1937
1361   TACTTTTTTC TTTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT          1987
1362   GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAAACTC TATTACTTTA          2037
1363   TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA          2087
1364   GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA          2137
1365   GTTATCAGAG TCT                                                  2150
1366
1367
1368
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1369   (2) INFORMATION FOR SEQ ID NO: 25:
1370        (i) SEQUENCE CHARACTERISTICS:
1371            (A) LENGTH:   2099 base pairs
1372            (B) TYPE:     nucleic acid
1373            (D) TOPOLOGY:  linear
1374        (ii) MOLECULE TYPE:  genomic DNA
1375        (ix) FEATURE:
1376            (A) NAME/KEY:  smage-II
1377        (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 25:
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1379
1380   ACCTTATTGG GTCTGTCTGC ATATGCCTCC ACTTGTGTGT AGCAGTCTCA          50
1381   AATGGATCTC TCTCTACAGA CCTCTGTCTG TGTCTGGCAC CCTAAGTGGC          100
1382   TTTGCATGGG CACAGGTTTC TGCCCCTGCA TGGAGCTTAA ATAGATCTTT          150
1383   CTCCACAGGC CTATACCCCT GCATTGTAAG TTTAAGTGGC TTTATGTGGA          200
1384   TACAGGTCTC TGCCCTTGTA TGCAGGCCTA AGTTTTTCTG TCTGCTTAGC          250
1385   CCCTCCAAGT GAAGCTAGTG AAAGATCTAA CCCACTTTTG GAAGTCTGAA          300
1386   ACTAGACTTT TATGCAGTGG CCTAACAAGT TTTAATTTCT TCCACAGGGT          350
1387   TTGCAGAAAA GAGCTTGATC CACGAGTTCG GAAGTCCTGG TATGTTCCTA          400
1388   GAAAGATGTT CTCCTGGAAA GCTTCAAAAG CCAGGTCTCC ATTAAGTCCA          450
1389   AGGTATTCTC TACCTGGTAG TACAGAGGTA CTTACAGGTT GTCATTCTTA          500
1390   TCTTTCCAGA TTCCTGTCTG CCAGCTCTTT TACTTCAGCC CTGAGCACAG          550
1391   TCAACATGCC TAGGGGTCAA AAGAGTAAGA CCCGCTCCCG TGCAAAACGA          600
1392   CAGCAGTCAC GCAGGGAGGT TCCAGTAGTT CAGCCCACTG CAGAGGAAGC          650
1393   AGGGTCTTCT CCTGTTGACC AGAGTGCTGG GTCCAGCTTC CCTGGTGGTT          700
1394   CTGCTCCTCA GGGTGTGAAA ACCCCTGGAT CTTTTGGTGC AGGTGTATCC          750
1395   TGCACAGGCT CTGGTATAGG TGGTAGAAAT GCTGCTGTCC TGCCTGATAC          800
1396   AAAAAGTTCA GATGGCACCC AGGCAGGGAC TTCCATTCAG CACACACTGA          850
1397   AAGATCCTAT CATGAGGAAG GCTAGTGTGC TGATAGAATT CCTGCTAGAT          900
1398   AAGTTTAAGA TGAAAGAAGC AGTTACAAGG AGTGAAATGC TGGCAGTAGT          950
1399   TAACAAGAAG TATAAGGAGC AATTCCCTGA GATCCTCAGG AGAACTTCTG          1000
1400   CACGCCTAGA ATTAGTCTTT GGTCTTGAGT TGAAGGAAAT TGATCCCAGC          1050
1401   ACTCATTCCT ATTTGCTGGT AGGCAAACTG GGTCTTTCCA CTGAGGGAAG          1100
1402   TTTGAGTAGT AACTGGGGGT TGCCTAGGAC AGGTCTCCTA ATGTCTGTCC          1150
1403   TAGGTGTGAT CTTCATGAAG GGTAACCGTG CCACTGAGCA AGAGGTCTGG          1200
1404   CAATTTCTGC ATGGAGTGGG GGTATATGCT GGGAAGAAGC ACTTGATCTT          1250
1405   TGGCGAGCCT GAGGAGTTTA TAAGAGATGT AGTGCGGGAA AATTACCTGG          1300
1406   AGTACCGCCA GGTACCTGGC AGTGATCCCC CAAGCTATGA GTTCCTGTGG          1350
1407   GGACCCAGAG CCCATGCTGA AACAACCAAG ATGAAAGTCC TGGAAGTTTT          1400
1408   AGCTAAAGTC AATGGCACAG TCCCTAGTGC CTTCCCTAAT CTCTACCAGT          1450
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INPUT SET: S32279.raw

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1409   TGGCTCTTAG AGATCAGGCA GGAGGGGTGC CAAGAAGGAG AGTTCAAGGC    1500
1410   AAGGGTGTTC ATTCCAAGGC CCCATCCCAA AAGTCCTCTA ACATGTAGTT    1550
1411   GAGTCTGTTC TGTTGTGTTT GAAAAACAGT CAGGCTCCTA ATCAGTAGAG    1600
1412   AGTTCATAGC CTACCAGAAC CAACATGCAT CCATTCTTGG CCTGTTATAC    1650
1413   ATTAGTAGAA TGGAGGCTAT TTTTGTTACT TTTCAAATGT TTGTTTAACT    1700
1414   AAACAGTGCT TTTTGCCATG CTTCTTGTTA ACTGCATAAA GAGGTAACTG    1750
1415   TCACTTGTCA GATTAGGACT TGTTTTGTTA TTTGCAACAA ACTGGAAAAC    1800
1416   ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA    1850
1417   TTGTCATGGC AATGTGATAT CATACAGTGG TGAAACAACA GTGAAGTGGG    1900
1418   AAAGTTTATA TTGTTAGTTT TGAAAATTTT ATGAGTGTGA TTGCTGTATA    1950
1419   CTTTTTTCTT TTTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA    2000
1420   CTTTACTCAA ATTCATTAGA AAGTAAATCA TAAAACTCTA TTACTTTATT    2050
1421   ATTTTCTTCA ATTATTAATT AAGCATTGGT TATCTGGAAG TTTCTCCAG     2099
1422
1423
1424
1425
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/819,669C*

DATE: 06/19/1999
TIME: 16:48:52

INPUT SET: S32279.raw

Line	Error	Original Text
30	Wrong Classification	(C) CLASSIFICATION: 435
73	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
96	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
152	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
168	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
212	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
332	Entered (2418) and Calc. Seq. Length (2419) differ	(A) LENGTH: 2418 base pairs
336	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
387	# of Sequences for line conflicts w/ running total	AATGATCTTG GGTGGATCC
393	Entered (5724) and Calc. Seq. Length (5674) differ	(A) LENGTH: 5724 base pairs
399	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
463	# of Sequences for line conflicts w/ running total	GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACC
531	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
635	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
664	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
717	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
753	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
824	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
894	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
934	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
950	# of Sequences for line conflicts w/ running total	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC A
951	# of Sequences for line conflicts w/ running total	CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG T
995	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
1060	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
1081	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
1136	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
1191	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
1238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
1274	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
1313	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
1328	# of Sequences for line conflicts w/ running total	ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT A
1329	# of Sequences for line conflicts w/ running total	AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG C
1346	# of Sequences for line conflicts w/ running total	GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT G
1347	# of Sequences for line conflicts w/ running total	CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA G
1377	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25: